

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 23, 2001, 10:49:24 : Search time 10.04 Seconds  
(without alignments)  
569.328 Million cell updates/sec

Title: US-09-195-368-1

Perfect score: 951

Sequence: 1 MCLSHLENPLSHSRTOGAQ.....VLKNNTYWCITILLANPQFIS 177

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	85.5	9.0	438	1	Y027_HUMAN	Q15049 homo sapien
2	77.5	8.1	880	1	ARG2_YEAST	P05085 saccharomyc
3	77	8.1	326	1	VS09_ROTTHA	P04328 human rotav
4	77	8.1	326	1	VS09_ROTTHD	P11850 human rotav
5	77	8.1	326	1	VS09_ROTTHH	P11851 human rotav
6	76.5	8.0	233	1	TNFA_FELCA	P19101 felis silve
7	76.5	8.0	233	1	TNFA_PAPHU	O77510 papio hamad
8	75	7.9	129	1	YF14_FOWP1	P21972 fowlopx vir
9	74.5	7.8	233	1	TNFA_PAPSP	P33620 papio sp. (
10	74.5	7.8	354	1	GRI_HOMAM	P41776 homarus ame
11	74	7.8	567	1	TRA3_MOUSE	Q60803 mus musculu
12	74	7.8	568	1	TRA3_HUMAN	Q13114 homo sapien
13	73.5	7.7	609	1	RFAL_XENLA	Q01588 xenopus lae
14	73	7.7	166	1	ING_SHEEP	P17773 ovis aries
15	73	7.7	326	1	VS09_ROTTHS	P04510 human rotav
16	73	7.7	1274	1	BXF_CLOBO	P30996 clostridium
17	72.5	7.6	233	1	TNFA_CANFA	P51742 canis famli
18	72.5	7.6	233	1	TNFA_MACFA	P79337 macaca fasc
19	72.5	7.6	233	1	TNFA_MACMU	P48094 macaca mula
20	72	7.6	234	1	TNFA_CAVPO	P51435 cavia porce
21	72	7.6	545	1	YB90_YEAST	P38346 saccharomyc
22	71.5	7.5	219	1	SPRA_IPOBA	P10917 ipomoea bat
23	71.5	7.5	233	1	TNFA_HUMAN	P01375 homo sapien
24	71.5	7.5	363	1	SD_DROME	P25722 drosophila
25	71	7.5	232	1	TNFA_PIG	P23563 sus scrofa
26	71	7.5	354	1	GBA3_USTHO	O14438 ustilago ho
27	71	7.5	354	1	GBA3_USTMA	P87034 ustilago ma
28	71	7.5	679	1	PBP2_STRPN	P10524 streptococc
29	70.5	7.4	352	1	GBA1_MAGGR	O13315 magnaporthe
30	70.5	7.4	890	1	BCN5_CLOPE	P08696 clostridium
31	70	7.4	1139	1	RBL2_HUMAN	Q08999 homo sapien
32	70	7.4	1323	1	ADRL_YEAST	P07248 saccharomyc
33	69.5	7.3	233	1	TNFA_MARMO	O35734 marmota mon

## ALIGNMENTS

### RESULT 1

Y027\_HUMAN STANDARD; PRT; 438 AA.  
AC Q15049;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE HYPOTHETICAL PROTEIN KIAA0027 (FRAGMENT).  
GN KIAA0027.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BONE MARROW;  
RX MEDLINE=96051387; PubMed=7584026;  
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayasi Y.,  
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;  
RT "Prediction of the coding sequences of unidentified human genes. I.  
RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by  
RT analysis of randomly sampled cDNA clones from human immature myeloid  
RT cell line KG-1.";  
RL DNA Res. 1:27-35(1994).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; D25217; BAA04947.1; -  
DR Hypothetical protein; Transmembrane.  
KW NON\_TER 1 1  
FT TRANSMEM 90 110 POTENTIAL.  
FT TRANSMEM 149 169 POTENTIAL.  
FT TRANSMEM 182 202 POTENTIAL.  
FT TRANSMEM 237 257 POTENTIAL.  
FT TRANSMEM 268 288 POTENTIAL.  
FT TRANSMEM 295 315 POTENTIAL.  
FT TRANSMEM 332 352 POTENTIAL.  
FT TRANSMEM 184 193 POLY-LEU.  
FT DOMAIN 210 213 POLY-LYS.  
FT DOMAIN 342 352 POLY-LEU.  
SQ SEQUENCE 438 AA; 46941 MW; B9A1001D1D8B8C08 CRC64;

Query Match 9.0%; Score 85.5; DB 1; Length 438;

Best Local Similarity 20.8%; Pred. No. 0.81; Indels 37; Gaps 6;

Matches 32; Conservative 31; Mismatches 54; Indels 37; Gaps 6;

QY 26 LWFPCSTVM--LLFLCSFSLIFLIFLQLETAKEPCMAKFGPLPSKQWMASSPEPCVKNKVS 83

DB 165 IFWGCKIVLPSAININFNILLLLELLMAATVITA-----ARSSEEDCKKK-- 212

QY 84 DHKLEILQGLLYIYGVAPNANNDVAPFEVRLYKKNKDMTQTLTKNSKIQNVGGTYELH 143  
 DB 213 -----KGSMSDSANILDEFPFARVLKSYSVVEVIAGISAV--LGGIILN 256  
 QY 144 VGDITDLIFNSHQVLKKNNTYGIILLANPOFIS 177  
 DB 257 VDHSV-----SGPHLSV---TFEWILLVACFPSAIA 283  
 RESULT 2  
 ARG2\_YEAST  
 ID ARG2\_YEAST STANDARD; PRT; 880 AA.  
 AC P05085;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE ARGININE METABOLISM REGULATION PROTEIN II.  
 GN ARG2 OR ARG81 OR YML099C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;  
 OC Saccharomycetaceae; Saccharomycetes.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86220196; PubMed=3709534;  
 RA Messenguy F., Dubois E., Descamps F.;  
 RT "Nucleotide sequence of the ARGRII regulatory gene and amino acid  
 RT sequence homologues between ARGRII PPRI and GAL4 regulatory  
 RL Eur. J. Biochem. 157:77-81(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;  
 RA Gentles S., Bowman S., Barrell B.G., Rajandream M.A.;  
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: THIS PROTEIN REPRESS OR INDUCES SEVERAL GENES OR  
 CC ARGININE METABOLISM.  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -!- SIMILARITY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR  
 CC CLUSTER DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; X03940; CAA27577.1; -;  
 DR EMBL; Z46660; CAA86638.1; -;  
 DR PIR; A25064; A25064.  
 DR TRANSPAC; T00044; -;  
 DR SGD; S0004565; ARG81.  
 DR INTERPRO; IPR001138; -;  
 DR PFAM; PF00172; Zn\_clus; 1.  
 DR PROSITE; PS00463; ZN2\_Cy6\_FUNGAL\_1; 1.  
 DR PROSITE; PS00048; ZN2\_Cy6\_FUNGAL\_2; 1.  
 DR Transcription regulation; Activator; DNA-binding; Nuclear protein;  
 KW Zinc; Metal-binding; Arginine metabolism.  
 FT DNA\_BIND 21 48 ZN(2)-CYS(6), FUNGAL-TYPE.  
 FT SIMILAR 587 690 TO N.CRASSA NMR (AA 96-193).  
 FT CONFLICT 4 4 S -> F (IN REF. 1).  
 FT CONFLICT 129 129 MISSING (IN REF. 1).  
 FT CONFLICT 283 283 F -> V (IN REF. 1).  
 FT CONFLICT 345 345 D -> V (IN REF. 1).  
 FT CONFLICT 366 366 E -> Q (IN REF. 1).  
 FT CONFLICT 549 549 T -> A (IN REF. 1).  
 FT CONFLICT 597 597 T -> S (IN REF. 1).  
 FT CONFLICT 665 665 K -> N (IN REF. 1).  
 FT CONFLICT 869 869 V -> I (IN REF. 1).  
 FT SEQUENCE 880 AA; 100281 MW; DA033AB2B373F415 CRC64;

Query Match 8.1%; Score 77.5; DB 1; Length 880;  
 Best Local Similarity 22.7%; Pred. No. 10;  
 Matches 37; Conservative 35; Mismatches 54; Indels 37; Gaps 8;  
 QY 45 IFIFLQL---ETAKEPCMAK-----FGPLPSKQWOMASSEPPCVNKV----- 82  
 DB 555 IFSLKLIQDSTALDKVRAKEIVILPSEEDNRYKPLDTSNATTSSEPRVDVYVQGLFRE 614  
 QY 83 -----SDWK---LEILQGLLYIYGVAPNAN---YNDVAPFEVRLYKKNKDMTQTLTKNSK 132  
 DB 615 ALNENDGKTHIEFVKPTNVSADSTPSSWTPIFNIA---TESYNKASDKLVSKTD 671  
 QY 133 IQNVGGTYELH-VGDTIDLIFNSEHQVLKKNNTYGIILLANPO 174  
 DB 672 -ENIIGTDSLYGLPNSLILLFSDCVIRVIRHNEYINLTPLVPR 713  
 DE GLYCOPROTEIN VP7 (SEROTYPE-SPECIFIC ANTIGEN) (OUTER SHELL  
 DE GLYCOPROTEIN).  
 GN S9.  
 OS Human rotavirus (serotype 2 / strain Hu5).  
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84221410; PubMed=6328448;  
 RA Dyall-Smith M.L., Holmes I.H.;  
 RT "Sequence homology between human and animal rotavirus  
 RT serotype-specific glycoproteins".  
 RL Nucleic Acids Res. 12:3973-3982(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88044489; PubMed=2823458;  
 RA Green K.Y., Midthun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
 RA Chanock R.M., Flores J.;  
 RT "Comparison of the amino acid sequences of the major neutralization  
 RT protein of four human rotavirus serotypes".  
 RL Virology 161:153-159(1987).  
 CC -!- FUNCTION: VP7 IS THE MAJOR NEUTRALISATION ANTIGEN.  
 CC -!- SUBCELLULAR LOCATION: ROUGH ENDOPLASMIC RETICULUM.  
 CC -----  
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 CC -----  
 DR EMBL; X00572; CAA25236.1; -;  
 DR EMBL; A01028; CAA00124.1; -;  
 DR PIR; G27620; VGXRHU.  
 DR PIR; A93520; VGXRHU.  
 DR INTERPRO; IPR001963; -;  
 DR PFAM; PF00434; VP7; 1.  
 DR Coat protein; Transmembrane; Glycoprotein.  
 KW TRANSMEM 32 48  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 326 AA; 37202 MW; 2D438F6EFC86FCB0 CRC64;  
 Query Match 8.1%; Score 77; DB 1; Length 326;  
 Best Local Similarity 22.8%; Pred. No. 3.6;  
 Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

VS09\_ROTTH STANDARD; PRT; 326 AA.  
 ID VS09\_ROTTH STANDARD; PRT; 326 AA.  
 AC P11851; 1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE GLYCOPROTEIN VP7 (SEROTYPE-SPECIFIC ANTIGEN) (OUTER SHELL  
 DE GLYCOPROTEIN)  
 GN S9  
 OS Human rotavirus (serotype 2 / strain HN126).  
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88044489; PubMed=2823458;  
 RA Green K.Y., Midthun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
 RA Chanock R.M., Flores J.;  
 RA "Comparison of the amino acid sequences of the major neutralization  
 RT protein of four human rotavirus serotypes.";  
 RL Virology 161:153-159(1987).  
 CC -1- FUNCTION: VP7 IS THE MAJOR NEUTRALISATION ANTIGEN.  
 CC -1- SUBCELLULAR LOCATION: ROUGH ENDOPLASMIC RETICULUM.  
 DR PIR: F27620: VGXRHN  
 DR INTERPRO: IPR001963; -  
 DR PFAM: PF00434; VP7; 1.  
 DR Coat protein; Transmembrane; Glycoprotein.  
 KW TRANSMEM 32 48  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 326 AA; 37246 MW; 4799219BE9D6A9B1 CRC64;

RESULT 4  
 VS09\_ROTTH STANDARD; PRT; 326 AA.  
 ID VS09\_ROTTH STANDARD; PRT; 326 AA.  
 AC P11850;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE GLYCOPROTEIN VP7 (SEROTYPE-SPECIFIC ANTIGEN) (OUTER SHELL  
 DE GLYCOPROTEIN)  
 GN S9  
 OS Human rotavirus (serotype 2 / strain DSI).  
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88044489; PubMed=2823458;  
 RA Green K.Y., Midthun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
 RA Chanock R.M., Flores J.;  
 RA "Comparison of the amino acid sequences of the major neutralization  
 RT protein of four human rotavirus serotypes.";  
 RL Virology 161:153-159(1987).  
 CC -1- FUNCTION: VP7 IS THE MAJOR NEUTRALISATION ANTIGEN.  
 CC -1- SUBCELLULAR LOCATION: ROUGH ENDOPLASMIC RETICULUM.  
 DR PIR: E27620: VGXRDS.  
 DR INTERPRO: IPR001963; -  
 DR PFAM: PF00434; VP7; 1.  
 DR Coat protein; Transmembrane; Glycoprotein.  
 KW TRANSMEM 32 48  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 326 AA; 37216 MW; 5D338B3BE9D6A9B5 CRC64;

Query Match 8.1%; Score 77; DB 1; Length 326;  
 Best Local Similarity 22.8%; Pred. No. 3.6;  
 Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;  
 QY 26 LWFCSIVMLFLC-----SFSWLIFLQLETAKEPCMAK-----FGPLPSKQWQ 71  
 DB 10 LTILISILLNVILKTTMTMDYIIFRELLLIALLISPFVTONYGMVLPITGSLDAVYTN 69  
 QY 72 ASSEPP-----CV-----NKVSDMKLEILQNGLYLYGOVAPNA---NYNDVAPFEV 115  
 DB 70 STSGEPFLTSLCLYYPAAKNEISDDDEWNTLSQLETKGWPISGVYFKDYNDINTFSV 129  
 QY 116 --RLYKNDMIOTLTNKSQIONGVGYELHVGDTIDLFNSEHQLVKNNTYWGIIILANP 173  
 DB 130 NPOLYCDYVNV-----LMRYDNTSELDASELADLIINE-----W-----LCNP 167  
 QY 174 QFIS 177  
 DB 168 MDIS 171  
 RESULT 5  
 VS09\_ROTTH STANDARD; PRT; 326 AA.  
 ID VS09\_ROTTH STANDARD; PRT; 326 AA.  
 AC P11850;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE GLYCOPROTEIN VP7 (SEROTYPE-SPECIFIC ANTIGEN) (OUTER SHELL  
 DE GLYCOPROTEIN)  
 GN S9  
 OS Human rotavirus (serotype 2 / strain DSI).  
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88044489; PubMed=2823458;  
 RA Green K.Y., Midthun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
 RA Chanock R.M., Flores J.;  
 RA "Comparison of the amino acid sequences of the major neutralization  
 RT protein of four human rotavirus serotypes.";  
 RL Virology 161:153-159(1987).  
 CC -1- FUNCTION: VP7 IS THE MAJOR NEUTRALISATION ANTIGEN.  
 CC -1- SUBCELLULAR LOCATION: ROUGH ENDOPLASMIC RETICULUM.  
 DR PIR: E27620: VGXRDS.  
 DR INTERPRO: IPR001963; -  
 DR PFAM: PF00434; VP7; 1.  
 DR Coat protein; Transmembrane; Glycoprotein.  
 KW TRANSMEM 32 48  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 326 AA; 37216 MW; 5D338B3BE9D6A9B5 CRC64;

VS09\_ROTTH STANDARD; PRT; 326 AA.  
 ID VS09\_ROTTH STANDARD; PRT; 326 AA.  
 AC P11851; 1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE GLYCOPROTEIN VP7 (SEROTYPE-SPECIFIC ANTIGEN) (OUTER SHELL  
 DE GLYCOPROTEIN)  
 GN S9  
 OS Human rotavirus (serotype 2 / strain HN126).  
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88044489; PubMed=2823458;  
 RA Green K.Y., Midthun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
 RA Chanock R.M., Flores J.;  
 RA "Comparison of the amino acid sequences of the major neutralization  
 RT protein of four human rotavirus serotypes.";  
 RL Virology 161:153-159(1987).  
 CC -1- FUNCTION: VP7 IS THE MAJOR NEUTRALISATION ANTIGEN.  
 CC -1- SUBCELLULAR LOCATION: ROUGH ENDOPLASMIC RETICULUM.  
 DR PIR: F27620: VGXRHN  
 DR INTERPRO: IPR001963; -  
 DR PFAM: PF00434; VP7; 1.  
 DR Coat protein; Transmembrane; Glycoprotein.  
 KW TRANSMEM 32 48  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 326 AA; 37246 MW; 4799219BE9D6A9B1 CRC64;

Query Match 8.1%; Score 77; DB 1; Length 326;  
 Best Local Similarity 22.8%; Pred. No. 3.6;  
 Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;  
 QY 26 LWFCSIVMLFLC-----SFSWLIFLQLETAKEPCMAK-----FGPLPSKQWQ 71  
 DB 10 LTILISILLNVILKTTMTMDYIIFRELLLIALLISPFVTONYGMVLPITGSLDAVYTN 69  
 QY 72 ASSEPP-----CV-----NKVSDMKLEILQNGLYLYGOVAPNA---NYNDVAPFEV 115  
 DB 70 STSGEPFLTSLCLYYPAAKNEISDDDEWNTLSQLETKGWPISGVYFKDYNDINTFSV 129  
 QY 116 --RLYKNDMIOTLTNKSQIONGVGYELHVGDTIDLFNSEHQLVKNNTYWGIIILANP 173  
 DB 130 NPOLYCDYVNV-----LMRYDNTSELDASELADLIINE-----W-----LCNP 167  
 QY 174 QFIS 177  
 DB 168 MDIS 171

RESULT 6  
 VS09\_ROTTH STANDARD; PRT; 326 AA.  
 ID VS09\_ROTTH STANDARD; PRT; 326 AA.  
 AC P11850;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE GLYCOPROTEIN VP7 (SEROTYPE-SPECIFIC ANTIGEN) (OUTER SHELL  
 DE GLYCOPROTEIN)  
 GN S9  
 OS Human rotavirus (serotype 2 / strain HN126).  
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88044489; PubMed=2823458;  
 RA Green K.Y., Midthun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
 RA Chanock R.M., Flores J.;  
 RA "Comparison of the amino acid sequences of the major neutralization  
 RT protein of four human rotavirus serotypes.";  
 RL Virology 161:153-159(1987).  
 CC -1- FUNCTION: VP7 IS THE MAJOR NEUTRALISATION ANTIGEN.  
 CC -1- SUBCELLULAR LOCATION: ROUGH ENDOPLASMIC RETICULUM.  
 DR PIR: F27620: VGXRHN  
 DR INTERPRO: IPR001963; -  
 DR PFAM: PF00434; VP7; 1.  
 DR Coat protein; Transmembrane; Glycoprotein.  
 KW TRANSMEM 32 48  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 326 AA; 37246 MW; 4799219BE9D6A9B1 CRC64;

QY 163 TWGIIILL 170  
I : I I I I  
Db 227 -YFGIIAL 233

RESULT 7  
TNFA\_PAPHU STANDARD; PRT: 233 AA.  
AC 077510;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).  
GN TNF OR TNFA.  
OS Papio hamadryas ursinus (Chacma baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Carnivora; Cercopithecoidea;  
OC Cercopithecinae; Papio.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98147379; PubMed=9488055;  
RA Haudek S.B., Redl H., Schlag G., Giroir B.P.;  
RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor  
RT alpha.";  
RL Mol. Immunol. 34:1041-1042(1997).  
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE  
CC WITH A WIDE VARIETY OF FUNCTIONS; IT CAN CAUSE CYTOLYSIS OF  
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
CC CONDITIONS.  
CC -1- SUBUNIT: HOMOTRIMER.  
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
CC EXTRACELLULAR SOLUBLE FORM.  
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
CC PROTEOLYTIC PROCESSING.  
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
CC AND MALNUTRITION.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
CC  
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CC -----  
CC EMBL: AF019963; AAC31675.1; -  
CC INTERPRO: IPR000478; -  
CC INTERPRO: IPR002959; -  
CC PFAM: PF00229; TNF; 1.  
CC PRINTS: PR01234; TNECROSISFCT.  
CC PRINTS: PR01235; TNFALPHA.  
CC PROSITE: PS00251; TNF\_1; 1.  
CC PROSITE: PS00049; TNF\_2; 1.  
CC Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.  
KW PROPEP 1 76  
FT CHAIN 77 233  
FT TRANSMEM 36 56  
FT DISULFID 145 177  
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT BY SIMILARITY.  
SQ SEQUENCE 233 AA; 25658 MW; B9403255058D4A03 CRC64;

Query Match 8.0%; Score 76.5; DB 1; Length 233;  
Best Local Similarity 21.8%; Pred. No. 2.8;  
Matches 50; Conservative 34; Mismatches 70; Indels 75; Gaps 11;

QY 7 ENMPLSHRTGAGRSSKWLFCISVIMLLFLCFSWLIIFL---QLETKPCMAKFG 63  
Db 15 EALPRKTAGQGSRR-CWFLSFLVLAGATLFCLLHGVIGQRFKPSL--IS 71

QY 64 PLPSKQMAS---SEPPCVN-----KVSDMKLEILQNGL 94  
 DB 72 PLAQAVERSSRTPSDKPVVHVANPOAQEGLOLWLNRRANALLANGVELDNLVVPSEGL 131  
 QY 95 YLIGQV-----APNANY---NDVAFPEVRLYKKNKMDIQTLTNKSIGN----- 135  
 DB 132 YLIQSVLFKGGQCPNSHVLLTHTISRIASVYQTKVNLLSAI--KSPCQRETPEGAEAKP 189  
 QY 136 -----VGGHYELHVGDTID-----LIFNSEHVLKNNYWGIIIL 170  
 DB 190 WYEPYILGVGVFQLEKGRDLSAEINLPDYLDFAESQGV-----YFGIIA 233  
 RESULT 8  
 YF14\_FOWP1 STANDARD; PRT; 129 AA.  
 AC P21972;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 DE HYPOTHETICAL 14.1 KDA PROTEIN.  
 GN F14.  
 OS Fowlpox virus (strain FP-1).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Avipoxvirus.  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90324937; PubMed=2165135;  
 RA Tartaglia J., Winslow J., Goebel S., Johnson G.P., Taylor J.,  
 RA Paoletti E.;  
 RT "Nucleotide sequence analysis of a 10.5 kbp HindIII fragment of  
 RT fowlpox virus: relatedness to the central portion of the vaccinia  
 RT virus HindIII D region."  
 RL J. Gen. Virol. 71:1517-1524 (1990).  
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 CC -----  
 DR EMBL; X62141; CAA44068.1; -  
 DR PIR; S22052; S22052.  
 DR HSSP; P01375; ITNF.  
 DR INTERPRO; IPR000478; -  
 DR INTERPRO; IPR002959; -  
 DR PFAM; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR PRINTS; PR01235; TNALPHA.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS0049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;  
 KW Myristate.  
 FT PROPEP 1 76 BY SIMILARITY.  
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR.  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 FT LIPID 19 19 MYRISTATE (BY SIMILARITY).  
 FT LIPID 20 20 MYRISTATE (BY SIMILARITY).  
 FT DISULFID 145 177 BY SIMILARITY.  
 SQ SEQUENCE 129 AA; 14110 MW; E0C25E79875E40DB CRC64;

Query Match 7.9%; Score 75; DB 1; Length 129;  
 Best Local Similarity 28.8%; Pred. No. 1.9;  
 Matches 23; Conservative 14; Mismatches 37; Indels 6; Gaps 3;

QY 31 SIYMLFLCFSWLIIFLQLETAKEPCMAKFGPLPSKQWQ---ASSEPPCVNKVSDWKL 87  
 DB 6 SIYLVTVIGSCFYNPFT-LTYECRDDCCNGRYGVPAPKVLNCTKTPGCPD--SGYLL 62  
 QY 88 EILONGLYLIYGOVAPNANY 107  
 DB 63 TTSENKTYCITGNETDKGY 82

RESULT 9  
 TNFA\_PAPSP STANDARD; PRT; 233 AA.  
 AC P33620;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).  
 GN TNF OR TNFA.  
 OS Papio sp. (Baboon).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Papio.  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RA Sanjanwala M., Edwards A.;  
 RL submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.  
 CC FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
 CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
 CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
 CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
 CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
 CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
 CC CONDITIONS.  
 CC SUBUNIT: HOMOTRIMER.  
 CC SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 CC PROTEOLYTIC PROCESSING.  
 CC SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X62141; CAA44068.1; -  
 DR PIR; S22052; S22052.  
 DR HSSP; P01375; ITNF.  
 DR INTERPRO; IPR000478; -  
 DR INTERPRO; IPR002959; -  
 DR PFAM; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR PRINTS; PR01235; TNALPHA.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS0049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;  
 KW Myristate.  
 FT PROPEP 1 76 BY SIMILARITY.  
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR.  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 FT LIPID 19 19 MYRISTATE (BY SIMILARITY).  
 FT LIPID 20 20 MYRISTATE (BY SIMILARITY).  
 FT DISULFID 145 177 BY SIMILARITY.  
 SQ SEQUENCE 233 AA; 25557 MW; 455360B48DC74173 CRC64;

Query Match 7.8%; Score 74.5; DB 1; Length 233;  
 Best Local Similarity 21.2%; Pred. No. 4.3;  
 Matches 51; Conservative 28; Mismatches 63; Indels 99; Gaps 12;

QY 7 ENMPLSHSRTOGAORSSWKLWLFCSIVMLFLCFSFWL-----IFIFLQL----- 51  
 DB 15 EALPKKTGGFGQSR-----CLFLSLFSLLVAGATFLFCLLHFGVIGPQRE 61  
 QY 52 ETAKPCMAKFGPLPSKQWQAS---SEPPCVNKVS----- 83  
 DB 62 EFPKDFSL--ISPLAQAVRSSRTPSDKPVHVANPOAQEGLOLWLNRRANALLANGVEL 119  
 QY 84 -DWKLEILONGLYLIYGOV-----APNANY---NDVAFPEVRLYKKNKMDIQTLTNKSII 133  
 DB 120 RDNQLVVPSEGLYIYSQVLFKGGQCPSTHVLTHTRISIAVSQYQTKVNLLSAI--KSPC 177  
 QY 134 QN-----VGGTYELHVGDTID-----LIFNSEHVLKNNYWGIIIL 169  
 DB 178 QRTPECAEAKPWYEPYILGVGVFQLEKGRDLSAEINLPDYLDFAESQGV-----YFGIIA 232  
 QY 170 L 170  
 DB 233 L 233

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RESULT 10
GBL_HOMAM STANDARD; PRT; 354 AA.
AC P41776;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1), ALPHA SUBUNIT (ADENYLATE
DE CYCLASE-INHIBITING G ALPHA PROTEIN).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OLFACTORY ORGAN;
RX MEDLINE=93061797; PubMed=1279345;
RA McClintock T.S., Byrnes A.P., Lerner M.R.;
RT "Molecular cloning of a G-protein alpha i subunit from the lobster
RT olfactory organ.";
RL Brain Res. Mol. Brain Res. 14:273-276(1992).
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 1
CC (G1/O/T/2).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S47614; CAB29288.1; ALT_SEQ.
DR PIR; A48976; A48976.
DR HSP; P10824; 1A33.
DR INTERPRO; IPR001019; -.
DR INTERPRO; IPR001408; -.
DR PFAM; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR PRINTS; PR00441; GPROTEINAI.
KW GTP-binding; Transducer; ADP-ribosylation; Multigene family;
KW Myristate.
FT INIT_MET 0 0 BY SIMILARITY.
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
FT NP_BIND 40 47 GTP (BY SIMILARITY).
FT NP_BIND 200 203 GTP (BY SIMILARITY).
FT NP_BIND 269 272 GTP (BY SIMILARITY).
FT MOD_RES 178 178 ADP-RIBOSYL[1] (BY ACTION OF CTX)
FT MOD_RES 351 351 (BY SIMILARITY).
FT MOD_RES 351 351 ADP-RIBOSYL[1] (BY ACTION OF IAP)
FT CONFLICT 308 323 MISSING (IN CAB29288).
FT SEQUENCE 354 AA; 40600 MW; 1A032BDCBF83896D CRC64;

Query Match 7.8%; Score 74.5; DB 1; Length 354;
Best Local Similarity 23.5%; Pred. No. 6.9;
Matches 36; Conservative 30; Mismatches 72; Indels 15; Gaps 6;

OY 18 GAORSSKWLWFC--SIYVLLFLCSFSLWIFLFIQLETAKE--PCMAKFGPL-PSKQOMA 72
DB 202 GQSRERKKNWCHCEGVTAIIIFVVALSGYDLVLAEDENMRNIESMKLFDSICNNKWFVE 261
OY 73 SSEPCVKNVSDWKLLEITLQNGLYLYIGQVAPNANYNDVAPFEVRLYKKNKMIQTLTKSK 132
DB 262 TSIIILFNKDLFEQIKTSPLTICFCFPGYQGSNVYEDSANYIRMKFEN-----LNKRK 314

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OY 133 IQNVGGTYELHWGDT--IDLIFNSEHOV-LKNN 162
DB 315 DQKELYTHFTCATDTNNIQFVDFDAVTDVTKNN 347

RESULT 11
TRA3_MOUSE STANDARD; PRT; 567 AA.
AC Q60803; Q62380;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1)
DE (CRAF1) (TRAFAMN).
CN TRAF3 OR CRAF1 OR TRAFAMN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signalling.";
RL Science 267:1494-1498(1995).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6J; TISSUE=BRAIN;
RX MEDLINE=96299439; PubMed=8660894;
RA Wang X., Bornslaeger E.A., Haub O., Tomihara-Newberger C., Lonberg N.,
RA Dinullos M.B., Distche C.M., Copeland N., Gilbert D.J., Jenkins N.A.,
RA Lacy E.;
RT "A candidate gene for the amniotless gastrulation stage mouse mutation
RT encodes a TRAF-related protein.";
RL Dev. Biol. 177:274-290(1996).
CC -!- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
CC TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
CC ASSOCIATED FACTORS (POTENTIAL).
CC -!- TISSUE SPECIFICITY: IN ADULT, HIGHEST IN BRAIN. ALSO FOUND IN
CC KIDNEY, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY. NOT
CC FOUND IN LIVER.
CC -!- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED FROM 6.5. HIGHEST
CC LEVELS FOUND BETWEEN E11.5 AND E13.5. AT LATE STAGES OF GESTATION,
CC FROM E14.5, ONLY LOW LEVELS ARE DETECTED.
CC -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC -!- SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.
CC -----
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CC -----
DR EMBL; U21050; AAC52175.1; -.
DR EMBL; U33840; AAC52710.1; -.
DR MGD; MGI:108041; TRAF3.
DR INTERPRO; IPR001841; -.
DR INTERPRO; IPR002083; -.
DR PFAM; PF00917; MATH; 1.
DR PFAM; PF00097; zf-C3HC4; 1.
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
DR Zinc-finger; Coiled coil.
DR ZN_FING 67 76 C3HC4-TYPE.
FT DOMAIN 266 337 COILED COIL (POTENTIAL).
FT DOMAIN 417 502 MATH/TRAF.
FT CONFLICT 72 73 CE -> WQ (IN REF. 2).
FT CONFLICT 390 390 "T -> M (IN REF. 2).
FT SEQUENCE 567 AA; 64263 MW; 2522B343B41192DC CRC64;

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Query Match          7.8%; Score 74; DB 1; Length 567;
Best Local Similarity 28.3%; Pred. No. 13;
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 72 ASSEPPCVNKVSDW-----KLEILQNGLYLYIGVAPNAN-----YNDVAFPEVRLYKNK 121
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 252 ASSAVQHVNLKWSNLSLEKKVSSLLQN-----ESVEKNKSQSLHNOICSFIEIERQK 305

QY 122 DMIQTITNKSKTQNGVGYELHVGDTIDLFNSEHQVLK 160
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 306 EMLR--NNESKI-----LHLQRLVID-----SQAELK 330

RESULT 12
TRA3_HUMAN
ID TRA3_HUMAN STANDARD; PRT; 568 AA.
AC Q13114; Q13076; Q13947; Q12990;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1)
DE (CRAF1) (CD40 BINDING PROTEIN) (CD40BP) (LMP1 ASSOCIATED PROTEIN)
DE (LAP1).
DE TRAF3 OR CRAF1 OR CAP-1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC [1]
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
RL Science 267:1494-1498 (1995).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX TISSUE=LYMPHOMA;
RA Mosialos G., Birkenbach M., Yalamanchili R., VanArsdale T., Ware C.,
RT Kieff E.;
RT "The Epstein-Barr virus transforming protein LMP1 engages signaling
RT proteins for the tumor necrosis factor receptor family.";
RL Cell 80:389-399 (1995).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=FETAL BRAIN;
RA Sato T., Irie S., Reed J.C.;
RT "A novel member of the TRAF family of putative signal transducing
RT proteins binds to the cytosolic domain of CD40.";
RL FEBS Lett. 358:113-118 (1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95073988; PubMed=7527023;
RA Hu H.M., O'Rourke K., Boguski M.S., Dixit V.M.;
RT "A novel RING finger protein interacts with the cytoplasmic domain of
RT CD40.";
RL J. Biol. Chem. 269:30069-30072 (1994).
CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
CC TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR.
CC -1- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
CC ASSOCIATED FACTORS (POTENTIAL).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC -1- SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.
CC -----
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Query Match          7.8%; Score 74; DB 1; Length 568;
Best Local Similarity 28.3%; Pred. No. 13;
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 72 ASSEPPCVNKVSDW-----KLEILQNGLYLYIGVAPNAN-----YNDVAFPEVRLYKNK 121
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 253 ASSAVQHVNLKWSNLSLEKKVSSLLQN-----ESVEKNKSQSLHNOICSFIEIERQK 306

QY 122 DMIQTITNKSKTQNGVGYELHVGDTIDLFNSEHQVLK 160
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 307 EMLR--NNESKI-----LHLQRLVID-----SQAELK 331

RESULT 13
REAL_XENLA
ID RFAL_XENLA STANDARD; PRT; 609 AA.
AC Q01588;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE REPLICATION PROTEIN A 70 KDA DNA-BINDING SUBUNIT (RP-A) (RF-A)
DE (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING
DE PROTEIN).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OC [1]
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=OOCYTE;
RA Adachi Y., Laemmli U.K.;
RT "Identification of nuclear pre-replication centers poised for DNA
RT synthesis in Xenopus egg extracts: immunolocalization study of
RT replication protein A.";
RL J. Cell Biol. 119:11-15 (1992).
CC -1- FUNCTION: ABSOLUTELY REQUIRED FOR SIMIAN VIRUS 40 DNA REPLICATION
CC IN VITRO. IT PARTICIPATES IN A VERY EARLY STEP IN INITIATION. RP-A
CC IS A SINGLE-STRANDED DNA-BINDING PROTEIN.
CC -1- SUBUNIT: HETEROTRIMER OF 70, 32, AND 14 KDA CHAINS. THE
CC DNA-BINDING ACTIVITY MAY RESIDE EXCLUSIVELY ON THE 70 KDA SUBUNIT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: TO OTHER SPECIES RPA2/RPA2.
CC -----
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FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 209 209 I -> T (IN REF. 2).
SQ SEQUENCE 326 AA; 37284 MW; 7688BC3877F79777 CRC64;

Query Match 7.7%; Score 73; DB 1; Length 326;
Best Local Similarity 22.3%; Pred. No. 8.7;
Matches 41; Conservative 30; Mismatches 59; Indels 54; Gaps 9;

OY 26 LWLFCSIVMLLFLC-----SFSWLIIFIFLOLETAKEPCMAK-----FGPLPSKWOM 71
| : ||| : : : ||| | : | : | :
Db 10 LTILISILLNYILKTITNTMDYIIERFLLIALISPFVYRTQNYGMYLPITGSLDAVYTN 69
OY 72 ASS-----EPPCV-----NKVSDMKLEILLQGLYLYGOVAPNA---NYNDVAPREV 115
: || : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 70 STGESFLWSTLCLYYPAAKAKNEISDEWENTLSQLFLTKGWPTGSVYFKDINDITTFSM 129
OY 116 --RLYKNKDMIQTLTNKSKIQNVGGTYELHVGDTIDLIENSEHQLKNNNTYWGIIILLANP 173
: || : : : : | : | : | : | : | : | : | : | : | : | : | : | :
Db 130 NPOLYCDYNVV-----LMRYDNTSELVDVSELADLILNE-----W-----LCNP 167

OY 174 OFTS 177
||
Db 168 MDIS 171

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Search completed: February 23, 2001, 10:51:11  
Job time: 107 sec

